

P:\OPER\IMPRO\ECODYSONE.CIP - 1/7/99

- 1 -

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

<120> NOVEL GENETIC SEQUENCES ENCODING STEROID AND JUVENILE HORMONE
5 RECEPTOR POLYPEPTIDES AND INSECTICIDAL MODALITIES THEREFOR II

<130> p:\oper\imro\ecdysone.cip

<140> US continuation-in-part of PCT/AU99/00033

<141> 1999-07-02

10 <150> PCT/AU/00033

<151> 1999-01-15

<150> AU PP1536

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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- 2 -

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Val Leu Ser Ser Asp Ile Asn Met Ser Pro Ser Ser Leu Asp Ser Pro
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Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr
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Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr
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Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
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aat tcc aat aat gcc tcc ctg aat aat caa aat caa aat tat caa aat 336
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Gly Leu Gly Gly Gly Ser Gln Val Asn Asn His Asn His Ser
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Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His
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His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu
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Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile
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5 aaa aaa ggt cct gcg ccc cgt tta caa gag gaa ctg tgt ctg gtg tgt 912
Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys
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cat cca acg tgt ccg ctg tta cct gaa gac att ttg gct aaa tgt caa 1296
10 His Pro Thr Cys Pro Leu Leu Pro Glu Asp Ile Leu Ala Lys Cys Gln
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gct cgt aat ata cct cct tta tcg tac aat caa ttg gca gtt ata tat 1344
Ala Arg Asn Ile Pro Pro Leu Ser Tyr Asn Gln Leu Ala Val Ile Tyr
15 435 440 445

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Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
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5 ttg cga atg gca cga cgt tac gat cac aat tca gat tcc ata ttc ttt 1632

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ctt acc gaa ctg cgt acg ttg ggc aat caa aat gcc gaa atg tgt ttc 1968

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Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile

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25 ggt ggt gcc gtc gat tat gtt ggc acc gat atg agt atg agt tta gta 2256

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caa tcg gat aat gca tag 2274

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35 40 45

Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr

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20

Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr

65 70 75 80

25 Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro

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Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn

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30 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val

115 120 125

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Gly Gly Gly Gly Gly Gly Val Pro Gly Met Thr Ser Leu Asn

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Gly Leu Gly Gly Gly Gly Ser Gln Val Asn Asn His Asn His Ser

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His Asn His Leu His His Asn Ser Asn Ser Asn His Ser Asn Ser Ser

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Leu Ser Val Asn Ile Asn Gly Pro Asn Ile Val Ser Asn Ala Gln Gln

195 200 205

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Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His His

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His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu

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25 Ser Ala Asn Ser Ile Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser

260 265 270

Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile

275 280 285

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Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys

- 10 -

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295

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Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly

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Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Cys

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330

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Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys

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Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro

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360

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15 Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys

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375

380

Lys Ala Gln Lys Glu Lys Asp Lys Ile Gln Thr Ser Val Cys Ala Thr

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390

395

400

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Glu Ile Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Ser

405

410

415

His Pro Thr Cys Pro Leu Leu Pro Glu Asp Ile Leu Ala Lys Cys Gln

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425

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Ala Arg Asn Ile Pro Pro Leu Ser Tyr Asn Gln Leu Ala Val Ile Tyr

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- 11 -

Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp

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Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln

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Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met

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Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe

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Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met

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Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile

580 585 590

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Phe Ser Asp Arg Pro Gly Leu Glu Glu Ala Glu Leu Val Glu Ala Ile

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Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His

30 610 615 620

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- 12 -

Cys Gly Asp Pro Met Ser Leu Val Phe Phe Ala Lys Leu Leu Ser Ile
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Leu Thr Glu Leu Arg Thr Leu Gly Asn 'Gln Asn Ala Glu Met Cys Phe
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Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
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Thr Gln Ala Glu Lys Ala Ala Gln Glu Ala Gln Ala Thr Thr Ser Ala
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20 Thr Ser Ser Ser Ser Ser Leu Ser Pro Ser Ala Ala Ser Thr Pro Asn
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 Pro Gln Glu Ile Lys Pro Asp Ile Ser Leu Leu Asn Glu Asn Asn Thr
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 Ser Ser Tyr Ser Pro Lys Pro Gly Ser Pro Asn Pro Phe Ala Ile Gly
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cac ccc ctt agt ggt tcg aaa cac ttg tgt tcc att tgt gga gac cgc 288
 His Pro Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg
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gcc agt gga aaa cat tat ggg gtc tac agt tgt gag ggt tgt aaa ggg 336
 Ala Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly
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 Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu
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 Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr
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	Gly Ala Gly Gly Gly Gly Gly Gly Val Ser Asn Val Val				
	180	185	190		
20	ggt gct ggc gga gaa gac ttt aaa ccc agc agt tca tta cgt gat ctc				624
	Gly Ala Gly Gly Glu Asp Phe Lys Pro Ser Ser Leu Arg Asp Leu				
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	Lys Gln Leu Tyr Gln Met Val Glu Tyr Ala Arg Arg Thr Pro His Phe				
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	Arg Arg Ser Pro Val Arg Gln Pro Gln Gln Leu Phe Leu Asn Gln Asn				
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	355 360 365	
15	atc gat cgc tcg gag ttg tcg tgt ctg aag gca atc ata ctc ttc aat	1152
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	Glu Lys Ile Tyr Ala Cys Leu Asp Glu His Cys Arg Thr Glu His Pro	
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- 16 -

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20 Gln Met Leu Gln Thr Thr Pro Pro Gln Gln Gln Gln Tyr Pro Pro Asn
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25 His Pro Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg
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30 Ala Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly
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35 Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu
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45 Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr
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85 Gln His Asp Tyr Lys Gly Ala Val Ser His Leu Cys Gln Met Val Asn
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90 Lys Gln Leu Tyr Gln Met Val Glu Tyr Ala Arg Arg Thr Pro His Phe

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- 17 -

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60	Ile Gly Glu Arg Ala Leu Glu Glu Leu Ile Ala Glu Gln Leu Glu Ala		
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Glu Phe Gly Thr Ser Ala Ile Val Asn Gly Phe Ile Arg Thr Ile Ser

1 5 10 15

15 ttg atc ctt att ctt ctt ctt ttt ctt ctt tgg agg ttg ttg gcc ttc 96
Leu Ile Leu Ile Phe Leu Leu Leu Phe Leu Trp Arg Leu Leu Ala Phe

20 25 30

20 cgg ttc ttg ttt ata tct gaa caa cca cct ccc gaa gag ctg tgc ctg 144
Arg Phe Leu Phe Ile Ser Glu Gln Pro Pro Pro Glu Glu Leu Cys Leu

35 40 45

25 gtc tgt ggc gac cgg tcc ggt tac cat tac aac gct ctc aca tgc 192
Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys

50 55 60

30 gaa gga tgc aag ggg ttc ttc cgg agg agc atc acc aag aac gcc gtc 240
Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val

65 70 75 80

tac cag tgc aag tac ggc aac aat tgc gaa atc gac atg tac atg agg 288

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- 19 -

Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr Met Arg

85

90

95

cgg aag tgc cag gag tgc cgg ctg aaa aaa tgc ctg acc gtc ggc atg 336

5 Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val Gly Met

100

105

110

agg cct gaa tgt gtt gta cct gaa gtt caa tgc gca gta aaa aga aag 384

Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys Arg Lys

10

115

120

125

gag aaa aaa gct caa cga gaa aaa gat aaa cca aat tct act aca gac 432

Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr Thr Asp

130

135

140

15

att tct cct gaa ata ata aaa ata gaa cct aca gag atg aag att gaa 480

Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys Ile Glu

145

150

155

160

20

tgt ggt gaa cca atg ata atg ggc aca cct atg ccg act gta cct tac 528

Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val Pro Tyr

165

170

175

gtg aaa cct ttg agt tct ctc gtg ccg aat tcg gca cga gtc acg ggt 576

25 Val Lys Pro Leu Ser Ser Leu Val Pro Asn Ser Ala Arg Val Thr Gly

180

185

190

tac aaa ttt

585

Tyr Lys Phe

30

195

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- 20 -

<210> 6

<211> 195

<212> PRT

5 <213> *Myzus persicae*

<400> 6

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Leu Ile Leu Ile Phe Leu Leu Leu Phe Leu Trp Arg Leu Leu Ala Phe

20 25 30

Arg Phe Leu Phe Ile Ser Glu Gln Pro Pro Pro Glu Glu Leu Cys Leu

15 35 40 45

Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys

50 55 60

20 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val

65 70 75 80

Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr Met Arg

85 90 95

25

Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val Gly Met

100 105 110

Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys Arg Lys

30 115 120 125

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- 21 -

Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr Thr Asp

130 135 140

Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys Ile Glu

5 145 150 155 160

Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val Pro Tyr

165 170 175

10 Val Lys Pro Leu Ser Ser Leu Val Pro Asn Ser Ala Arg Val Thr Gly

180 185 190

Tyr Lys Phe

195

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<210> 7

<211> 208

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<213> Myzus persicae

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ctgtgaaggc tgtaagggtt tctttcgacg gagtgttacc aaaaatgcgg tgtattgttg 120

25

taaatttgggt catgcctgacg aaatggacat gtatatgcga cgtaaatgtc aggaatgtag 180

gctgaaaaaaaaa tgtttggctg tgggcattg 208

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35 <213> Myzus persicae

<400> 8

catgcggcccg gaatgtgtgg tgcccgaaaa ccagtgtgca atgaaacgac gcgaaaaagaa 60

- 22 -

agcacaaaaa gagaaggata aaatacagac cagtgtgtgt gcaacggaaa taaaaagga 120

aataactcgat ttaatgacat gtgaacccgc atcacatcca acgtgtccgc ttttacctga 180

5 agacattttg gctaaatgtc aagtcgtaa tatacctcct ttatcgatca atcaattggc 240

agttatataat aaattaatat ggtatcaaga tggctacgaa cagccatccg aggaagatct 300

10 caaacgtata atgagttcac ccgatgaaaa taaaagtcaa cacgtgcac catttgcac 360

tataacagaa atcaactatac taacatgtaca attaattgtt gaatgtgcac aaggtctagg 420

gtaccgagct cgaatt 436

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20 <211> 1797

<212> DNA

25 <213> *Myzus persicae*

<220>

30 <221> CDS

<222> (1)..(1797)

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1 5 10 15

45

gcc gcc ggt atc ggt ggc ggc ggt gtc ggc ggc ctc atg tcg tac aac 96

Ala Ala Gly Ile Gly Gly Gly Val Gly Gly Leu Met Ser Tyr Asn

50 20 25 30

55

cgt ggc cgt ggc acc gag gtc atc atc aaa ccc cgt agt cct gcc 144

Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala

35 40 45

60

gtg gtg cag gtg gcc acc ggt ggc agt tac cac ggc ctg ccg ggc gcc 192

65 Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala

50 55 60

70

tcc gac gcc gtc atc gtg cgc agc ccg cca ggc ggc cac ttg ccc ggg 240

Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly

75 65 70 75 80

ccg cag cag caa gtg ccg ccg tcc cgc aac ggc tgc tcc acc ctg ttt 289

- 23 -

Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
 85 90 95

5 agc gac atc gtc aag cga ctc agg ccc gac gat tgg ttg gcc 336
 Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
 10 100 105 110

15 gtc aac tcg ccc gcc tct tcg ccc ggc acg tcg cac ata tcc tac 384
 Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
 20 115 120 125

25 aca gtc ata tcg aac ggc ggc ggt ggc ggc ggt ggc ggt ggt 432
 Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140

30 tac aac acg tct cca atg tcg acc aac acg tac gac ccc tac agt ccc 480
 Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
 35 145 150 155 160

40 atg agt gga aaa atc gtc aaa gaa gag ttg tct ccg cca aac acg ctg 528
 Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
 165 170 175

45 tcg gga gtc agc agc cat tcg gat ggg ttg aag aag aag aaa ctc aac 576
 Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Leu Asn
 50 180 185 190

55 cac acg ccc tcg acc ggt gtc gtc aac acc tcg gca tcg ggc ccc ggg 624
 His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
 60 195 200 205

65 ggt ggc gtt ggt ggc aat gtg ctg aac aac cga cct ccc gaa gag ctg 672
 Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
 210 215 220

70 tgc ctg gtg tgt ggc gac cgg tcg tcc ggt tac cat tac aac gct ctc 720
 Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
 75 225 230 235 240

80 aca tgc gaa gga tgc aag ggg ttc ttc cgg agg acg atc acc aag aac 768
 Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn
 245 250 255

85 gcc gtg tac cag tgc aag tac ggc aac aat tgc gaa atc gac atg tac 816
 Ala Val Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr
 90 260 265 270

- 24 -

	aeg agg cgg aag tgc cag gag tgc cgg ctg aaa aaa tgc ctg acc gtc	864
5	Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val	
	275 280 285	
10	ggc atg agg cct gaa tgt gtt gta cct gaa gtt caa tgc gca gta aaa	912
	Gly Met Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys	
15	290 295 300	
20	aga aag gag aaa aaa gct caa cga gaa aaa gat aaa cca aat tct act	960
	Arg Lys Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr	
	305 310 315 320	
25	aca gac att tct cct gaa ata ata aaa ata gaa cct aca gag atg aag	1008
	Thr Asp Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys	
30	325 330 335	
35	att gaa tgt ggt gaa cca atg ata atg ggc aca cct atg ccc act gta	1056
	Ile Glu Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val	
40	340 345 350	
45	cct tac gtg aaa cct ttg agt tct gaa caa aaa gaa ctg atc cac cga	1104
	Pro Tyr Val Lys Pro Leu Ser Ser Glu Gln Lys Glu Leu Ile His Arg	
	355 360 365	
50	ctt gtc tat ttc cag gat caa tat gaa gct cct agt gaa aaa gac atg	1152
	Leu Val Tyr Phe Gln Asp Gln Tyr Glu Ala Pro Ser Glu Lys Asp Met	
55	370 375 380	
60	aaa cgt tta aca ata aat aat caa aat atg gat gaa tat gat gaa gaa	1200
	Lys Arg Leu Thr Ile Asn Asn Gln Asn Met Asp Glu Tyr Asp Glu Glu	
	385 390 395 400	
65	aaa caa agt gac acc aca tat cga atc atc act gag atg aca ata ctc	1248
	Lys Gln Ser Asp Thr Thr Tyr Arg Ile Ile Thr Glu Met Thr Ile Leu	
70	405 410 415	
75	aca gtt caa ctg att gtt gag ttt gcc aaa cga tta cca ggt ttc gat	1296
	Thr Val Gln Leu Ile Val Glu Phe Ala Lys Arg Leu Pro Gly Phe Asp	
80	420 425 430	
85	aaa ctt gta aga gaa gat caa atc act tta ctc aag gct tgc tca agt	1344
	Lys Leu Val Arg Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser	
	435 440 445	
90	gaa gct atg atg ttc agg gta gca agg aag tat gac atc acc act gac	1392

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- 25 -

Glu Ala Met Met Phe Arg Val Ala Arg Lys Tyr Asp Ile Thr Thr Asp
 450 455 460
 5
 tca ata gtg ttt gct aac aac cag cca ttt tca gct gat tca tat aac 1440
 Ser Ile Val Phe Ala Asn Asn Gln Pro Phe Ser Ala Asp Ser Tyr Asn
 10 465 470 475 480
 15 aaa gct gga ttg gga gat gcc att gaa aac caa ctg tca ttc agt cgg 1488
 Lys Ala Gly Leu Gly Asp Ala Ile Glu Asn Gln Leu Ser Phe Ser Arg
 20 485 490 495
 25 ttt atg tac aat atg aag gtg gat aac gca gaa tat gcc tta ttg acc 1536
 Phe Met Tyr Asn Met Lys Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr
 500 505 510
 30 gcc atc gtc ata ttt tcg agt agg cca aat tta cta gat ggt tgg aaa 1584
 Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys
 35 515 520 525
 40 gtg gag aaa atc caa gaa atc tac cta gag tcc tta aaa gct tat gta 1632
 Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val
 530 535 540
 45 gat aat cga gac cgt gac aca gca act gta cga tat gcg cga ctt ctc 1680
 Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu
 545 550 555 560
 55 tca gta ctt aca gaa ttg cgc aca tca ggc aat gaa aac tct gag cta 1728
 Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu
 565 570 575
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 65 ttt atg aca ctg aaa ctg aaa aac aga gta gta ccc cca ttc ttg gcc 1776
 Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala
 580 585 590
 70 gaa ata tgg gat gtc atg cca 1797
 Glu Ile Trp Asp Val Met Pro
 75 595
 80 <210> 10
 <211> 599
 85 <212> PRT
 <213> *Myzus persicae*
 90 <400> 10

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-26-

Met Met Asp Gln Lys Cys Asp Val Gly Gly Gly Val Ala Ala Ala
1 5 10 15

5 Ala Ala Gly Ile Gly Gly Val Gly Gly Leu Met Ser Tyr Asn
10 20 25 30

15 Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala
35 40 45

20 Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala
50 55 60

25 Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly
65 70 75 80

30 Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
85 90 95

35 Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
100 105 110

40 Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
115 120 125

45 Thr Val Ile Ser Asn Gly
130 135 140

50 Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
145 150 155 160

55 Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
165 170 175

60 65 Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Leu Asn
180 185 190

70 His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
195 200 205

75 80 Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
210 215 220

85 Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
225 230 235 240

90 Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn

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	245	250	255
5	Ala Val Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr		
	260	265	270
10	Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val		
	275	280	285
15	Gly Met Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys		
	290	295	300
20	Arg Lys Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr		
	305	310	315
	320		
30	Thr Asp Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys		
	325	330	335
35	Ile Glu Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val		
	340	345	350
40	Pro Tyr Val Lys Pro Leu Ser Ser Glu Gln Lys Glu Leu Ile His Arg		
	355	360	365
45	Leu Val Tyr Phe Gln Asp Gln Tyr Glu Ala Pro Ser Glu Lys Asp Met		
	370	375	380
50	Lys Arg Leu Thr Ile Asn Asn Gln Asn Met Asp Glu Tyr Asp Glu Glu		
	385	390	395
	400		
60	Lys Gln Ser Asp Thr Thr Tyr Arg Ile Ile Thr Glu Met Thr Ile Leu		
	405	410	415
65	Thr Val Gln Leu Ile Val Glu Phe Ala Lys Arg Leu Pro Gly Phe Asp		
	420	425	430
70	Lys Leu Val Arg Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser		
	435	440	445
75	Glu Ala Met Met Phe Arg Val Ala Arg Lys Tyr Asp Ile Thr Thr Asp		
	450	455	460
80	Ser Ile Val Phe Ala Asn Asn Gln Pro Phe Ser Ala Asp Ser Tyr Asn		
	465	470	475
	480		
85	Lys Ala Gly Leu Gly Asp Ala Ile Glu Asn Gln Leu Ser Phe Ser Arg		
	485	490	495

- 28 -

Phe Met Tyr Asn Met Lys Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr
5 500 505 510

Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys
10 515 520 525

Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val
15 530 535 540

Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu
20 545 550 555 560

Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu
25 565 570 575

Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala
30 580 585 590

Glu Ile Trp Asp Val Met Pro
35 595

<210> 11
40 <211> 1131
45 <212> DNA
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55 <220>
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Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser
70 1 5 10 15

gtc gat cgg aac agt atg atg aat aat tct tgc aac gta caa gac tct 96
75 Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
80 20 25 30

cgg aat tac ccc aac cat cca ctc agc ggt tcg aaa cat ctg tgc 144
85 Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
85 35 40 45

tcc ata tgc ggc gat cgc gcc agt gga aaa cat tac gga gtc tac agc 192
90 Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser

- 29 -

	50	55	60	
5	tgc gag ggg tgc aaa ggg ttc ttc aaa cgc aca gtg agg aaa aat ttg			240
	Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu			
10	65	70	75	80
15	tca tac gcg tgt cgc gaa gaa aac aaa tgc atc atc gac aag cgc caa			288
	Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln			
	85	90	95	
20	cga aat cgg tgc caa tac tgc agg tat caa aaa tgt ttg acc atg ggc			336
	Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly			
25	100	105	110	
30	atg aaa aga gaa gct gtg cag gaa gaa aga caa cgt aca aaa gaa cga			384
	Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg			
	115	120	125	
35	gat cat aat aac atc gaa gtt gaa ccc acg agc agt tct aat act gat			432
	Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp			
40	130	135	140	
45	atg cca gtg gaa ctc ata tta agg gct gag aat aaa gct gat gct ata			480
	Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile			
50	145	150	155	160
55	aag act gaa caa cag tat ata gag caa cga cat cct caa cat act gtt			528
	Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val			
	165	170	175	
60	ggt gct att tgt caa gca act gac aag cag tta ata caa ctt gtt gaa			576
	Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu			
65	180	185	190	
70	tgg gcc aag cat ata ccg cat ttt aaa aat tta cct cta ggc gat caa			624
	Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln			
	195	200	205	
75	gtt tta tta ttg aga gct ggt tgg aat gag ttg atg att gca gca ttt			672
	Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe			
80	210	215	220	
85	tec eat aga tca atc agt gta aaa gat ggt ata gtc tta gct act gga			720
	Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly			
90	225	230	235	240

- 30 -

ctt act gtt gac aga gat tca gct cac caa gct ggt gtt gaa gct ata 768
 Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile
 5 245 250 255

ttt gat cgt gta ctc act gaa ctc gtt gct aaa atg aga gat atg ggt 816
 Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly
 10 260 265 270

atg gat aga aca gag ctt ggc tgt ttg cgt act att att ctt ttt aat 864
 Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn
 15 275 280 285

cca ggt tca aaa ggt ttg cag tct gtg aat gaa gtg caa gta ctg cgt 912
 Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg
 20 290 295 300

gat aag gtt tat gtt gcg tta gaa gaa tat tgt cgt aca aca cat cca 960
 Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro
 25 305 310 315 320

gaa gaa cct gga cga ttt gct aaa cta ctt ctt cgg ctt cct tca tta 1008
 Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
 30 325 330 335

cgt tca att gga tta aaa tgt ctg gaa cat tta ttc ttt tat aaa ctt 1056
 Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu
 35 340 345 350

att ggc gat tcc cca att gat aca ttt tta atg gaa gtt ctc gaa tca 1104
 Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser
 40 355 360 365

tct tca cat gac gtt caa gta gct aca 1131
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 45 370 375

<210> 12
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 50 <213> Myzus persicae

<400> 12
 Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser
 55 1 5 10 15

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- 31 -

Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
20 25 30

5 Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
10 35 40 45

15 Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser
50 55 60

20 Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu
65 70 75 80

25 Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln
85 90 95

30 Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly
100 105 110

35 Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg
40 115 120 125

45 Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Asn Thr Asp
130 135 140

50 Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile
145 150 155 160

55 Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val
165 170 175

60 Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu
180 185 190

65 Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln
70 195 200 205

75 Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe
210 215 220

80 Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly
225 230 235 240

85 Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile
245 250 255

90 Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly

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260

265

270

5 Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn
275 280 285

10 Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg
290 295 300

15 Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro
305 310 315 320

20 Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
25 325 330 335

30 Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu
340 345 350

35 Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser
355 360 365

40 Ser Ser His Asp Val Gln Val Ala Thr
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45

<210> 13

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50 <213> *Lucilia cuprina*

<220>

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55

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Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp

1 5 10

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ttg aca tat gct tgt cgt gag gac aat tgc att ata gat aaa cga 98

- 33 -

Leu Thr Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg

15

20

25

30

caa aga aat cgt tgc cag tat tgc cgc tac caa aag tgatcgatac cgtcga 150

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35

40

<210> 14

10 <211> 42

<212> PRT

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